```
1     AGCAGACAGAGGACTCTCATTAAGGAAGG TGTCCTGTGCCCTGACCCTACAAGATGCCA   59
                                                          MetPro      2

60    AGAGAAGATGCTCACTTCATCTATGGTTAC CCCAAGAAGGGGCACGGCCACTCTTACACC  119
3     ArgGluAspAlaHisPheIleTyrGlyTyr ProLysLysGlyHisGlyHisSerTyrThr   22

120   ACGGCTGAAGAGGCCGCTGGGATCGGCATC CTGACAGTGATCCTGGGAGTCTTACTGCTC  180
23    ThrAlaGluGluAlaAlaGlyIleGlyIle LeuThrValIleLeuGlyValLeuLeuLeu   43

181   ATCGGCTGTTGGTATTGTAGAAGACGAAAT GGATACAGAGCCTTGATGGATAAAAGTCTT  239
44    IleGlyCysTrpTyrCysArgArgArgAsn GlyTyrArgAlaLeuMetAspLysSerLeu   62

240   CATGTTGGCACTCAATGTGCCTTAACAAGA AGATGCCCACAAGAAGGGTTTGATCATCGG  300
63    HisValGlyThrGlnCysAlaLeuThrArg ArgCysProGlnGluGlyPheAspHisArg   83

301   GACAGCAAAGTGTCTCTTCAAGAGAAAAAC TGTGAACCTGTGGTTCCCAATGCTCCACCT  359
84    AspSerLysValSerLeuGlnGluLysAsn CysGluProValValProAsnAlaProPro  102

360   GCTTATGAGAAACTCTCTGCAGAACAGTCA CCACCACCTTATTCACCTTAAGAGCCAGCG  420
103   AlaTyrGluLysLeuSerAlaGluGlnSer ProProProTyrSerPro              118

421   AGACACCTGAGACATGCTGAAATTATTTCT CTCACACTTTTGCTTGAATTTAATACAGAC  479
```

FIG. 1A

#4

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```
480   ATCTAATGTTCTCCTTTGGAATGGTGTAGG AAAAATGCAAGCCATCTCTAATAATAAGTC   540
541   AGTGTTAAAATTTTAGTAGGTCCGCTAGCA GTACTAATCATGTGAGGAAATGATGAGAAA   599
600   TATTAAATTGGGAAAACTCCATCAATAAAT GTTGCAATGCATGATACTATCTGTGCCAGA   660
661   GGTAATGTTAGTAAATCCATGGTGTTATTT TCTGAGAGACAGAATTCAAGTGGGTATTCT   719
720   GGGGCCATCCAATTTCTCTTTACTTGAAAT TTGGCTAATAACAAACTAGTCAGGTTTTCG   780
781   AACCTTGACCGACATGAACTGTACACAGAA TTGTTCCAGTACTATGGAGTGCTCACAAAG   839
840   GATACTTTTACAGGTTAAGACAAAGGGTTG ACTGGCCTATTTATCTGATCAAGAACATGT   900
901   CAGCAATGTCTCTTTGTGCTCTAAAATTCT ATTATACTACAATAATATATTGTAAAGATC   959
960   CTATAGCTCTTTTTTTTTGAGATGGAGTTT CGCTTTTGTTGCCCAGGCTGGAGTGCAATG  1020
1021  GCGCGATCTTGGCTCACCATAACCTCCGCC TCCCAGGTTCAAGCAATTCTCCTGCCTTAG  1079
1080  CCTCCTGAGTAGCTGGGATTACAGGCGTGC GCCACTATGCCTGACTAATTTTGTAGTTTT  1140
1141  AGTAGAGACGGGGTTTCTCCATGTTGGTCA GGCTGGTCTCAAACTCCTGACCTCAGGTGA  1199
1200  TCTGCCCGCCTCAGCCTCCCAAAGTGCTGG AATTACAGGCGTGAGCCACCACGCCTGGCT  1260
1261  GGATCCTATATCTTAGGTAAGACATATAAC GCAGTCTAATTACATTTCACTTCAAGGCTC  1319
1320  AATGCTATTCTAACTAATGACAAGTATTTT CTACTAAACCAGAAATTGGTAGAAGGATTT  1380
1381  AAATAAGTAAAAGCTACTATGTACTGCCTT AGTGCTGATGCCTGTGTACTGCCTTAAATG  1439
1440  TACCTATGGCAATTTAGCTCTCTTGGGTTC CCAAATCCCTCTCACAAGAATGTGCAGAAG  1500
1501  AAATCATAAAGGATCAGAGATTCTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAA  1559
```

FIG. 1B

0000000 - 1000000

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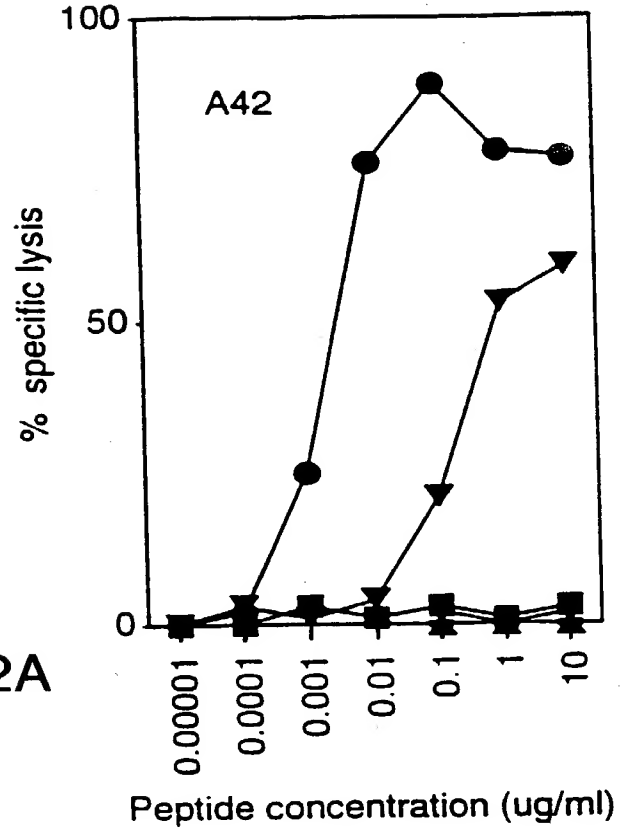

FIG. 2A

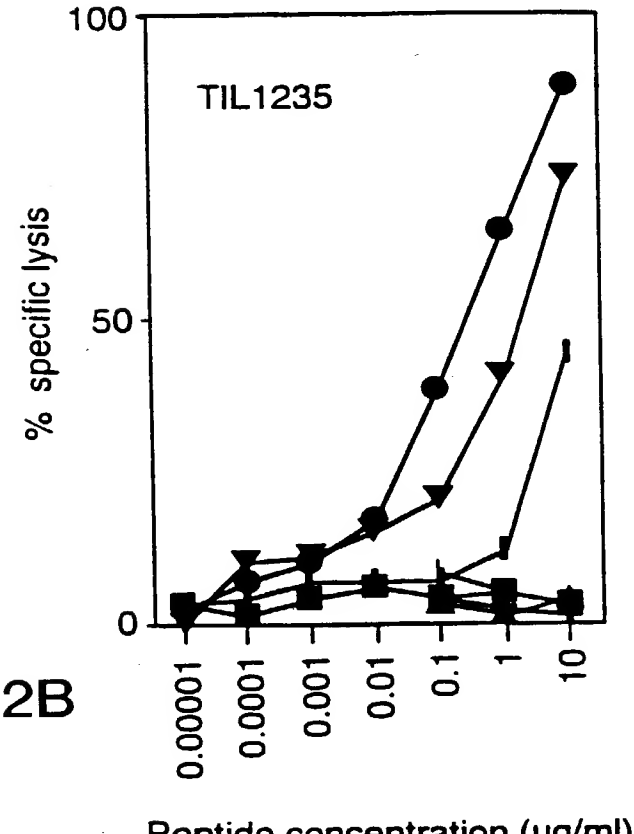

FIG. 2B

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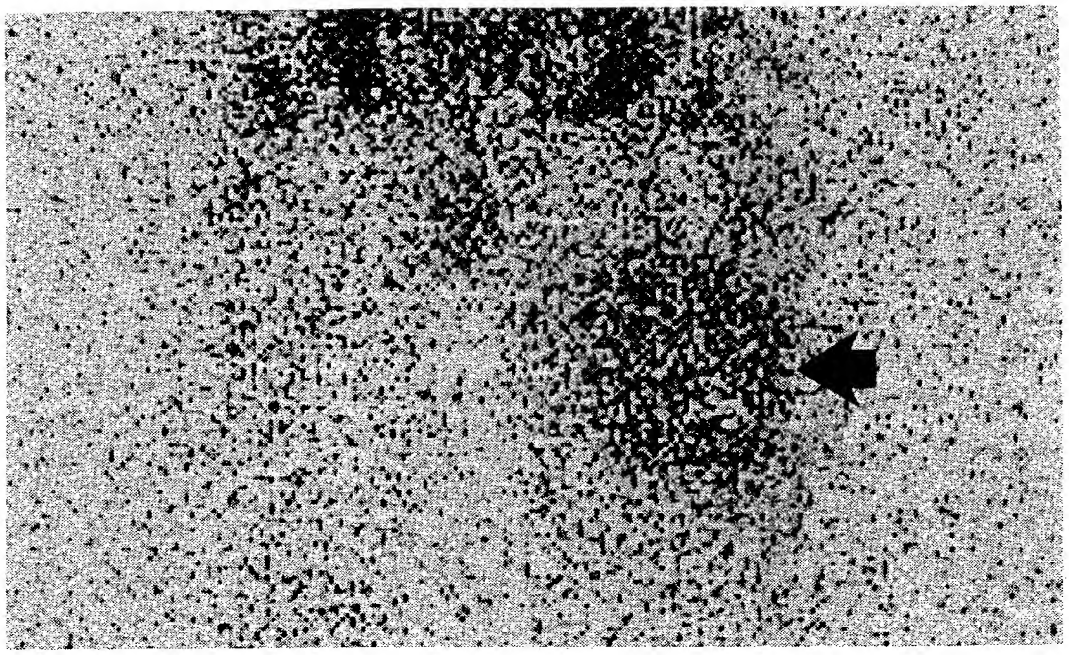

FIG. 3A

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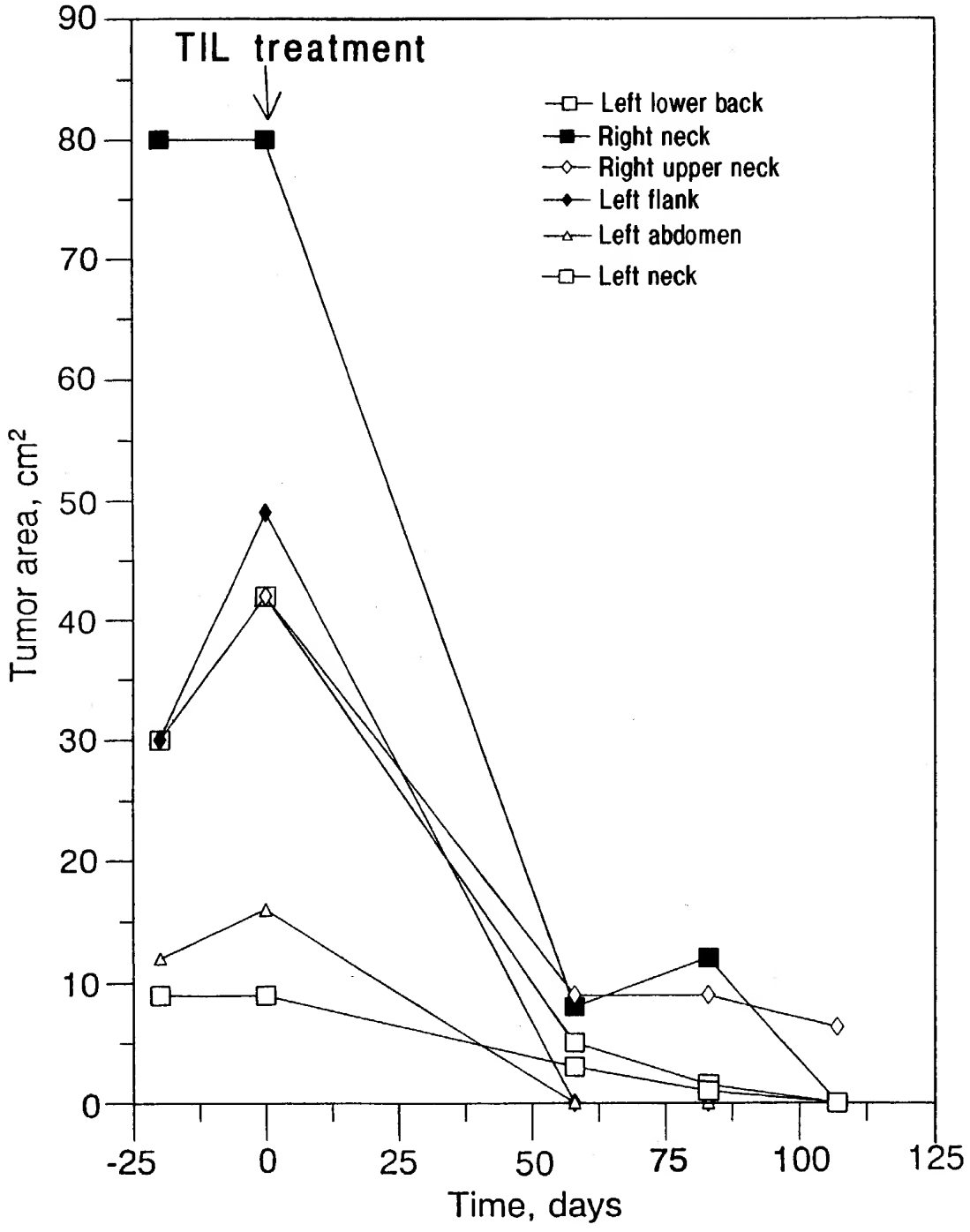


FIG. 3B

09898860 .101684

GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT 40

GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG 80

ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA 120

GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC 160

CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA 200

GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC 240

TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA 280

TGCCTCCTTC TCTATTGCCT TGAACTTCCC TGGAAGCCAA 320

AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA 360

CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT 400

GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT 440

GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA 480

GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA 520

ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA 560

GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGACTG 600

TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC 640

TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT 680

TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG 720

GGAACAAGCA CTTCCTGAGA AATCAGCCTC TGACCTTTGC 760

CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT 800

GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA 840

CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT 880

GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT 920

GCCATTCCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG 960

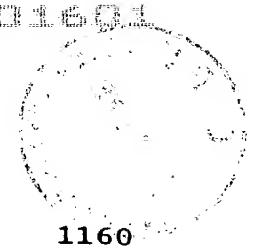
GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCCTAA 1000

CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT 1040

ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA 1080

CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC 1120

FIG. 4A



TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG	1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA	1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC	1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA	1280
GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG	1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC	1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG	1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA	1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG	1480
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA	1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG	1560
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC	1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG	1640
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC	1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG	1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC	1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG	1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG	1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG	1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC	1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC	1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC	2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG	2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC	2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT	2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA	2160
AAAAAAAAAA AA	2172

FIG. 4B

0989860 .101601

```
  1  MDLVLKRCLL HLAVIGALLA VGATKVPRNQ DWLGVSRQLR TKAWNRQLYP
 51  EWTEAQRLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLPDG
101  QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
151  YVWKTWGQYW QFLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
201  AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY
251  LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS
301  CGSSPVPGTT DGHRPTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGTTS
351  VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
401  TPAEVSIVVL SGTTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
451  TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
501  AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQRL CQPVLPSPAC
551  QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
601  GILLVLMAVV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG
651  ENSPLLSGQQ V
```

FIG. 5A

```
Pmel17      M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20        M-----V-----Q-----L----- .....------------
gp100       M-----V-----Q-----L-----.....------------
cDNA25FL    M-----F-----Q-----L-----.....------------
cDNA25TR                  Q-----L-----.....-----PPQWAAGLSTLI
            1     162    236    274    588          649
```

FIG. 5B

09898860.101601

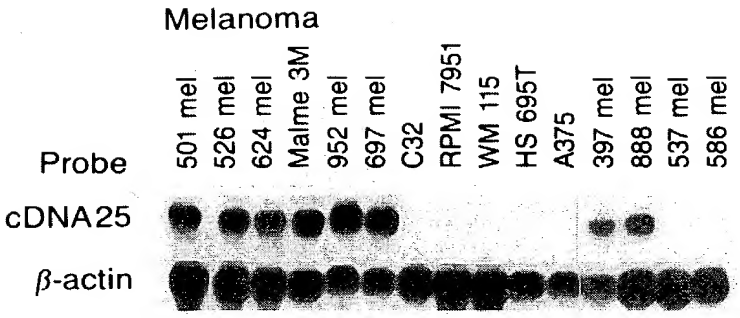


FIG. 6A

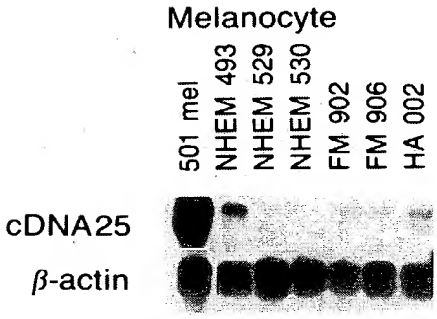


FIG. 6B

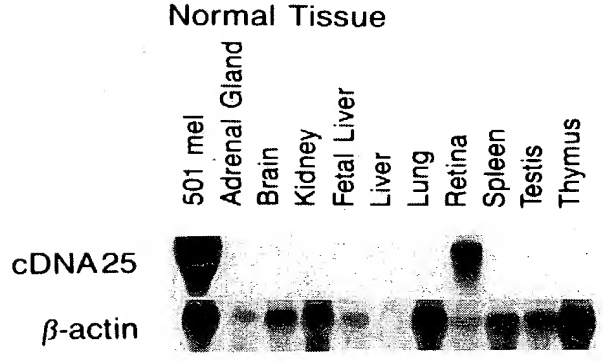


FIG. 6C